

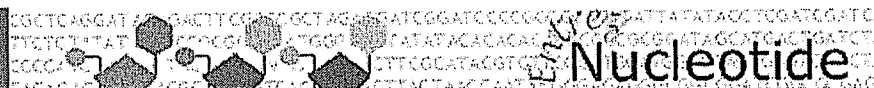
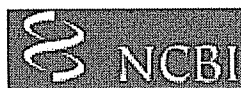
PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
(Case No. 02-1270-A)

In application of)	
)	
J. Fruehauf, <i>et al.</i>)	Examiner: Lei Yao
)	
Serial No. 10/734,880)	
)	Group Art Unit: 1642
Filed: December 12, 2003)	
)	
For: Gene Related Sensitivity and Resistance)	Confirmation No.: 1031
To Chemotherapeutic Drug Treatment)	

Commissioner for Patents
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Alexandria, VA 22313-14501

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APPENDIX B



Nucleotide
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Search for

Display Show Hide: ☐ sequence ☐ all but gene, CDS and mRNA features

Range: from to ☐ Reverse complemented strand Features: ☐ SNP

☐ 1: [AF458589](#). Reports Homo sapiens myos...[gi:21360805]

[Links](#)

[Features](#) [Sequence](#)

LOCUS AF458589 4631 bp mRNA linear PRI 10-JUN-2002
DEFINITION Homo sapiens myosin phosphatase target subunit 1 variant (PPP1R12A)
mRNA, complete cds.
ACCESSION AF458589
VERSION AF458589.1 GI:21360805
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4631)
AUTHORS Guo,J.H., Chen,X.Y. and Yu,L.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-2001) School of Life Sciences, Institute of
Genetics, Fudan University, Handan Road, 220, Shanghai 200433,
China

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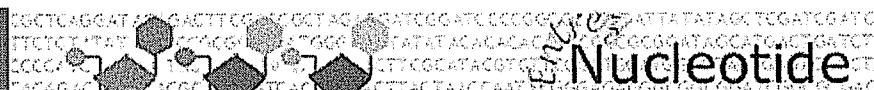

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Search for

Display Show Hide: ☐ sequence ☐ all but gene, CDS and mRNA features

Range: from to ☐ Reverse complemented strand Features:

☐ 1: [U79283](#). Reports Human albumin D-b...[gi:1710256]

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[Features](#) [Sequence](#)

LOCUS HSU79283 1480 bp mRNA linear PRI 28-NOV-2000
DEFINITION Human albumin D-box binding protein mRNA, complete cds.
ACCESSION U79283
VERSION U79283.1 GI:1710256
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1480)
AUTHORS Andersson,B., Wentland,M.A., Ricafrente,J.Y., Liu,W. and Gibbs,R.A.
TITLE A 'double adaptor' method for improved shotgun library construction
JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)
PUBMED 8619474
REFERENCE 2 (bases 1 to 1480)
AUTHORS Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W.,
Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.
TITLE Large-scale concatenation cDNA sequencing
JOURNAL Genome Res. 7 (4), 353-358 (1997)
PUBMED 9110174
REFERENCE 3 (bases 1 to 1480)
AUTHORS Yu,W. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Submitted (22-NOV-1996) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
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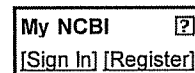
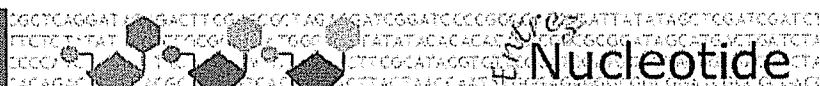
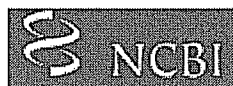
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Search for Display Show Send to Hide: ☐ sequence ☐ all but gene, CDS and mRNA featuresRange: from to ☐ Reverse complemented strand Features: ☐ SNP ☒ MGC ☐ 1: BC063851. Reports Homo sapiens comp...[gi:39645842]

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LOCUS BC063851 4015 bp mRNA linear PRI 15-JUL-2006

DEFINITION Homo sapiens complement component 7, mRNA (cDNA clone MGC:75123 IMAGE:6184213), complete cds.

ACCESSION BC063851

VERSION BC063851.1 GI:39645842

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4015)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRM Mammalian Gene Collection Program Team

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED [12477932](#)

REFERENCE 2 (bases 1 to 4015)

CONSRM NIH MGC Project

TITLE Direct Submission

JOURNAL Submitted (08-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
 Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave

Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 141 Row: d Column: 14
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 45580687.

Differences found between this sequence and the human reference genome (build 36) are described in misc_difference features below.

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CDS	96..2627 /gene="C7" /codon_start=1 /product="complement component 7" /protein_id="AAH63851.1" /db_xref="GI:39645843" /db_xref="GeneID:730" /db_xref="HGNC:1346" /db_xref="MIM:217070" /translation="MKVISLFLVGFIFGFQSFSSASSPVNCQWDFYAPWSECNGCTK TQTRRRSVAVYGQYGGQPCVGNFETQSCEPTRGCPTEEGCGERFRFCFSGQCISKSLV CNGDSDCEDSADEDRCEDSERRPSCDIDKPPPNIELTGNGYNELTGQFRNRVINTKS FGGQCRKVFSGDGKDFYRLSGNVLSYTFQVKINNDFNIEFYNSTWSYVKHTSTEHTSS SRKRSFFRSSSSSRYSYTSHTNEIHKGSYQLLVVENTVEVAQFINNNPEFLQLAEPF WKELSHLPSLYDYSAYRRLIDQYGTHYLQSGSLGGEYRVLFYVDSEKLRQDNFNSVEE KKKSSGWHFVVKFSSHGCKELENALKAASGTQNNVLRGEFFIRGGGAGFISGLSYLE LDNPAGNKRRYSAWAESVTNLQVIKQKLTPLYELVKEVPCASVKKLYLKWALEEYLD EFDPCCHRPCQNGGLATVEGTHCLCHCKPYTFGAACEQGVLVGNQAGGVDDGWSCWSS WSPCVQGGKTRSRCCNNPPPSGGGRSCVGETTESTQCEDELEHLRLLEPHCFPLSLV PTEFCPSPPALKDGFVQDEGTMFPVGVKNVYTCNEGYSLIGNPVARCGEDLRWLVGEM HCQKIACVLPVLMGDIQSHPPQKPFYTVGEKVTVSCSGGMSLEGPSAFLCGSSLKWSPE MKNARCQKENPLTQAVPKCQRWEKLNQNSRCVCKMPYECGSLDVCAQDERSKRIPLP TVCKMHVLHCQGRNYTLTGRDSTLPASAEKACGACPLWGKCDAAESSKVCREASECE EEGFSICVEVNGKEQTMSECEAGALRCRGSISVTSIRPCAAETQ"
misc difference	3994..4015 /gene="C7" /note="polyA tail: 22 bases do not align to the human genome."

ORIGIN

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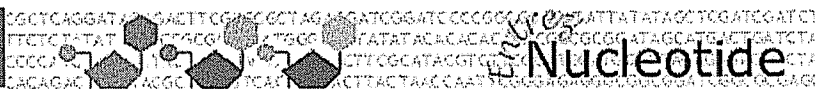
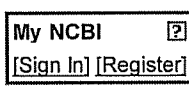


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Last update: Mon, 12 Jan 2009 Rev. 149544

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☐ 1: BC002788. Reports Homo sapiens plas...[gi:33877182]

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Comment Features Sequence

LOCUS BC002788 1353 bp mRNA linear PRI 15-JUL-2006
 DEFINITION Homo sapiens plasminogen activator, urokinase receptor, mRNA (cDNA clone MGC:3905 IMAGE:3617894), complete cds.
 ACCESSION BC002788
 VERSION BC002788.2 GI:33877182
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1353)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 CONSRTM Mammalian Gene Collection Program Team
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1353)
 CONSRTM NIH MGC Project
 TITLE Direct Submission
 JOURNAL Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT On Aug 19, 2003 this sequence version replaced gi:12803884.
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 12 Row: j Column: 13
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 53829377.

Differences found between this sequence and the human reference genome (build 36) are described in misc_difference features below.

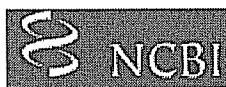
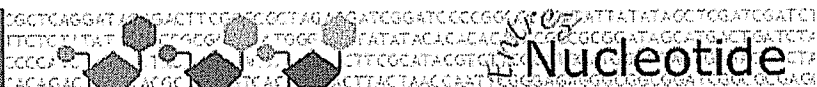
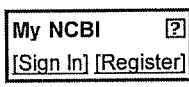
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Comment Features Sequence

LOCUS BC005235 1199 bp mRNA linear PRI 15-JUL-2006
 DEFINITION Homo sapiens nuclear DNA-binding protein, mRNA (cDNA clone MGC:12261 IMAGE:3930648), complete cds.
 ACCESSION BC005235
 VERSION BC005235.1 GI:13528872
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1199)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 CONSRTM Mammalian Gene Collection Program Team
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1199)
 CONSRTM NIH MGC Project
 TITLE Direct Submission
 JOURNAL Submitted (27-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 16 Row: 1 Column: 7
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27894372.

Differences found between this sequence and the human reference genome (build 36) are described in misc_difference features below and these differences were also compared to chimpanzee genome (build 2).

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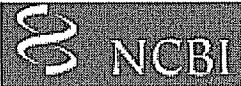
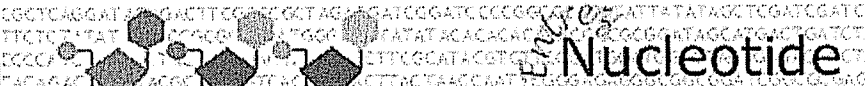
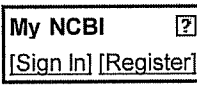
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Last update: Mon, 12 Jan 2009 Rev. 149544

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP

☐ 1: [AF060181](#). Reports Homo sapiens zinc...[gi:3228539]

[Links](#)

[Features](#) [Sequence](#)

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 AUTHORS Still, I.H.
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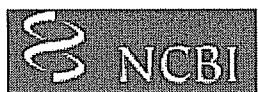
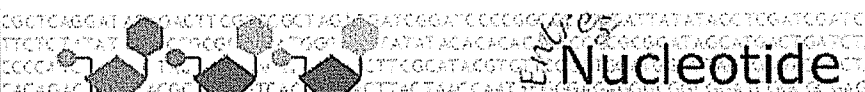
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Search for

Display Show Hide: ☐ sequence ☐ all but gene, CDS and mRNA features

Range: from to ☐ Reverse complemented strand Features:

☐ 1: [AF237631](#). Reports Homo sapiens ubiq...[gi:7288860]

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[Features](#) [Sequence](#)

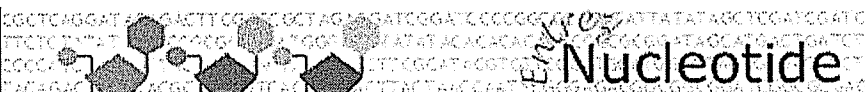
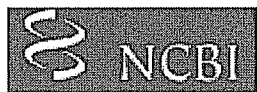
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 JOURNAL Mol. Biol. Cell 9, 18A (1998)
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☐ 1: [D00099](#). Reports Homo sapiens mRNA...[gi:219941]

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LOCUS HUMNKATPA 4108 bp mRNA linear PRI 11-MAR-1998
DEFINITION Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds.
ACCESSION D00099
VERSION D00099.1 GI:219941
KEYWORDS Na,K-ATPase; alpha-subunit.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4108)
AUTHORS Kawakami,K., Ohta,T., Nojima,H. and Nagano,K.
TITLE Primary structure of the alpha-subunit of human Na,K-ATPase deduced
from cDNA sequence
JOURNAL J. Biochem. 100 (2), 389-397 (1986)
PUBMED [2430951](#)
COMMENT The alpha-subunit of the human Na,K-ATPase exhibited 87% homology
with its Torpedo counterpart and 98% homology with its sheep
counterpart.
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polyA signal

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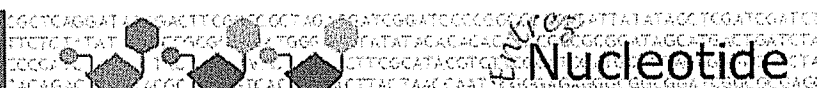
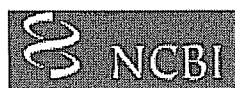
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☐ 1: BC002795. Reports Homo sapiens plas...[gi:33877195]

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LOCUS BC002795 2409 bp mRNA linear PRI 19-MAR-2007
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 ACCESSION BC002795
 VERSION BC002795.2 GI:33877195
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2409)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 CONSRTM Mammalian Gene Collection Program Team
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED [12477932](#)
 REFERENCE 2 (bases 1 to 2409)
 CONSRTM NIH MGC Project
 TITLE Direct Submission
 JOURNAL Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT On Aug 19, 2003 this sequence version replaced gi:12803896.
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 12 Row: p Column: 15
~~This clone was selected for full length sequencing because it~~
passed the following selection criteria: matched mRNA gi: 14702165.

Differences found between this sequence and the human reference genome (build 36) are described in misc_difference features below.

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